

Applicants' Attorney requests an extension of time to respond to the Notice. A Petition for Extension of Time and the appropriate fees are being filed concurrently.

Transmitted herewith is a copy of the "Sequence Listing" (sheets 1/4 through 4/4) in paper form for the above-identified patent application as required by 37 C.F.R. §1.821(c) and a copy of the "Sequence Listing" in computer readable form as required by 37 C.F.R. §1.821(e). As required by 37 C.F.R. §1.821(f), Applicants' Attorney hereby states that the content of the "Sequence Listing" in paper form and the computer readable form of the "Sequence Listing" are the same and, as required by 37 C.F.R. §1.821(g), also states that the submission includes no new matter.

Applicants' Attorney submits the following amendments to comply with 37 C.F.R. §1.825:

In the Specification

Please insert the attached "Sequence Listing" (sheets 1/4 through 4/4), and comprising SEQ ID NOS: 1-22, into the above-referenced application.

Please replace the paragraph at page 5, line 20, with the following:

a2 - - Figs. 1A and 1B show the results of fine mapping of chromosome 9. - - -

Please replace the paragraph at page 5, lines 21-22, with the following:

a3 - - Figs. 2A-2D show the results of an association study performed on 204 cases and 117 controls. - - -

Please replace the paragraph at page 32, lines 6-13, with the following:

a4 --- An initial whole genome scan was performed on 167 individuals from 22 families. This allowed the identification of four chromosomal regions with NPL scores greater than 1.60. One of these peaks (NPL score = 2.35) was at D9S925. Using the GeneMap '98 (<http://www.ncbi.nlm.nih.gov/genemap/>), it was determined that the VLDLr gene locus was located within 23 cM of D9S925. In subsequent fine mapping of this region with 21 additional families and six additional markers from the region, the peak shifted to D9S285, and the NPL value increased to 2.79. This marker is estimated to be about 20 cM from the VLDLr locus (Figs. 1A and 1B).--

Please replace the paragraph at page 33, lines 5-12, with the following:

a5 --- In the Chicoutimi case-control cohort, the major alleles had repeat sizes of 5, 8 and 9, which accounted for 98% of all alleles. Minor alleles with repeat sizes of 7, 10 and 11 were seen in this population. In the association study, performed on 204 cases and 117 controls, it was determined that individuals who are homozygous for five repeats, the "5/5 genotype", have a reduced susceptibility to CHD (odds ratio of 0.55 at the 0.046 significance level) (see Figs. 2A-2D). The case control study also found odds ratios of 1.45 and 1.60 for the 8/8 and the 8/9 genotypes, respectively, but neither of these results was statistically significant.--